

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/908,943B
Source: IFW/6
Date Processed by STIC: 2-4-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/04/2005

PATENT APPLICATION: US/09/908,943B

TIME: 15:33:40

Input Set : A:\00281AUS.txt

Output Set: N:\CRF4\02042005\I908943B.raw

4 <110> APPLICANT: Yan, Riqiang
5 Tomasselli, Alfredo G.
6 Gurney, Mark E.
7 Emmons, Thomas L.
8 Bienkowski, Mike J.
9 Heinrikson, Robert L.
11 <120> TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
13 <130> FILE REFERENCE: 29915/00281A.US
15 <140> CURRENT APPLICATION NUMBER: 09/908,943B
16 <141> CURRENT FILING DATE: 2001-07-19
18 <150> PRIOR APPLICATION NUMBER: 60/219,795
19 <151> PRIOR FILING DATE: 2000-07-19
21 <160> NUMBER OF SEQ ID NOS: 199
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2070
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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32 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc ccccttgggg 120
33 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
34 gtggagatgg tggacaacct gaggggcaag tgggggagc gctactacgt ggagatgacc 240
35 gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
36 gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
37 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
38 ctgggcaccg acctggttaag catcccccat ggccccaaag tcaactgtgc tgccaacatt 480
39 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacacctg 540
40 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
41 ctggtaaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgcgggcttc 660
42 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720
43 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780
44 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
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46 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
47 ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
48 ttcccagtc tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
49 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
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51 ggcttctacg ttgtctttga tggggccga aaacgaattg gctttgctgt cagcgcttgc 1260
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54 gtcattggctg ccatctgcgc cctcttcatt ctgccactct gcctcatggt gtgtcagtg 1440

(pg. 6-7)

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55 cgctgcctcc gctgcctgcg ccagcagcat gatgactttg ctgatgacat ctccctgctg 1500
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57 ctttggtcac aagtaggaga cacagatggc acctgtggcc agagcacctc aggaccctcc 1620
58 ccaccacca aatgcctctg cttgatgga gaaggaaaag gctggcaagg tgggttccag 1680
59 ggactgtacc ttaggaaac agaaaagaga agaaagaagc actctgctgg cgggaatact 1740
60 cttggtcacc tcaaatttaa gtctggaaat tctgctgctt gaaacttcag ccctgaacct 1800
61 ttgtccacca ttcttttaa ttctccaacc caaagtattc ttcttttctt agtttcagaa 1860
62 gtactggcat cacacgcagg ttacctggc gtgtgtccct gtggtaccct ggcagagaag 1920
63 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
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68 <211> LENGTH: 501
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
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76 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
77 20 25 30
79 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
80 35 40 45
82 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
83 50 55 60
85 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
86 65 70 75 80
88 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
89 85 90 95
91 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
92 100 105 110
94 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
95 115 120 125
97 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
98 130 135 140
100 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
101 145 150 155 160
103 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
104 165 170 175
106 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
107 180 185 190
109 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
110 195 200 205
112 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
113 210 215 220
115 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
116 225 230 235 240
118 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
119 245 250 255
121 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln

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Input Set : A:\00281AUS.txt

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125          275          280          285
127 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
128          290          295          300
130 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
131 305          310          315          320
133 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
134          325          330          335
136 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
137          340          345          350
139 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
140          355          360          365
142 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
143          370          375          380
145 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
146 385          390          395          400
148 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
149          405          410          415
151 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
152          420          425          430
154 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
155          435          440          445
157 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
158          450          455          460
160 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
161 465          470          475          480
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166 Ile Ser Leu Leu Lys
167          500
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171 <211> LENGTH: 1977
172 <212> TYPE: DNA
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 3
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178 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
179 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
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181 gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360
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183 ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480
184 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540
185 gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct 600
186 gaagtgtctg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660
187 acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt gatcattgtg 720
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191 gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcatctca 960
192 ctctacctaa tgggtgaggt taccaaccag tccttccgca tcaccatcct tccgcagcaa 1020
193 tacctgcggc cagtgggaaga tgtggccacg tcccaagacg actgttataa gtttgccatc 1080
194 tcacagtcac ccacgggcac tggtatggga gctgttatca tggagggtt ctacgttgtc 1140
195 tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
196 ttcaggacgg cagcgggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260
197 aacattccac agacagatga gtcaaccctc atgaccatag cctatgtcat ggctgccatc 1320
198 tgcgccctct tcatgctgcc actctgcctc atgggtgtgtc agtggcgctg cctccgctgc 1380
199 ctgcgccagc agcatgatga ctttctgat gacatctccc tgctgaagtg aggaggccca 1440
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203 gaaacagaaa agagaagaaa gaagcactct gctggcgagg atactcttgg tcacctcaaa 1680
204 ttaagtgcg gaaattctgc tgcttgaaac ttcagccctg aacctttgtc caccattcct 1740
205 ttaaattctc caacccaaag tattcttctt ttcttagttt cagaagtact ggcacacac 1800
206 gcaggttacc ttggcgtgtg tccctgtggt accctggcag agaagagacc aagcttgttt 1860
207 ccctgctggc caaagtcagt aggagaggat gcacagtttg ctatttgctt tagagacagg 1920
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210 <210> SEQ ID NO: 4

211 <211> LENGTH: 476

212 <212> TYPE: PRT

213 <213> ORGANISM: Homo sapiens

215 <400> SEQUENCE: 4

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220           20           25           30
222 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
223           35           40           45
225 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
226           50           55           60
228 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
229           65           70           75           80
231 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
232           85           90           95
234 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
235           100          105          110
237 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
238           115          120          125
240 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
241           130          135          140
243 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
244           145          150          155          160
246 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
247           165          170          175
249 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
250           180          185          190

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252 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
253      195      200      205
255 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
256      210      215      220
258 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
259 225      230      235      240
261 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
262      245      250      255
264 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
265      260      265      270
267 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
268      275      280      285
270 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
271      290      295      300
273 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
274 305      310      315      320
276 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
277      325      330      335
280 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
281      340      345      350
283 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
284      355      360      365
286 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
287      370      375      380
289 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
290 385      390      395      400
292 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
293      405      410      415
295 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
296      420      425      430
298 Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
299      435      440      445
301 Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
302      450      455      460
304 His Asp Asp Phe Ala Asp Ile Ser Leu Leu Lys
305 465      470      475
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309 <211> LENGTH: 14
310 <212> TYPE: PRT
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
315 peptide sequence
317 <400> SEQUENCE: 5
318 Lys Val Glu Ala Asn Tyr Glu Val Glu Gly Glu Arg Lys Lys
319 1      5      10
322 <210> SEQ ID NO: 6
323 <211> LENGTH: 15
324 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 7
Seq#:15; Xaa Pos. 4,7
Seq#:16; Xaa Pos. 1,4,5,6,7
Seq#:17; Xaa Pos. 1,2,4,5,6,7
Seq#:18; Xaa Pos. 1,2,4,5,6,7
Seq#:21; Xaa Pos. 5
Seq#:27; Xaa Pos. 7,19
Seq#:28; Xaa Pos. 6,7,11,20
Seq#:41; Xaa Pos. 9
Seq#:49; Xaa Pos. 1
Seq#:50; Xaa Pos. 2
Seq#:51; Xaa Pos. 3
Seq#:52; Xaa Pos. 4
Seq#:53; Xaa Pos. 5
Seq#:54; Xaa Pos. 6
Seq#:55; Xaa Pos. 7
Seq#:56; Xaa Pos. 8
Seq#:57; Xaa Pos. 1
Seq#:58; Xaa Pos. 2
Seq#:59; Xaa Pos. 3
Seq#:60; Xaa Pos. 4
Seq#:61; Xaa Pos. 5
Seq#:62; Xaa Pos. 6
Seq#:63; Xaa Pos. 7
Seq#:64; Xaa Pos. 8
Seq#:65; Xaa Pos. 1
Seq#:66; Xaa Pos. 2
Seq#:67; Xaa Pos. 3
Seq#:68; Xaa Pos. 4
Seq#:69; Xaa Pos. 5
Seq#:70; Xaa Pos. 6
Seq#:71; Xaa Pos. 7
Seq#:72; Xaa Pos. 8
Seq#:73; Xaa Pos. 1
Seq#:74; Xaa Pos. 2
Seq#:75; Xaa Pos. 3
Seq#:76; Xaa Pos. 4
Seq#:77; Xaa Pos. 7
Seq#:78; Xaa Pos. 8
Seq#:79; Xaa Pos. 8
Seq#:80; Xaa Pos. 9
Seq#:81; Xaa Pos. 1,7
Seq#:82; Xaa Pos. 2,7
Seq#:83; Xaa Pos. 3,7

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Seq#:84; Xaa Pos. 4,7
Seq#:85; Xaa Pos. 5,7
Seq#:86; Xaa Pos. 6,7
Seq#:87; Xaa Pos. 7
Seq#:88; Xaa Pos. 7,8
Seq#:89; Xaa Pos. 1
Seq#:90; Xaa Pos. 1,2

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L:473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:925 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1099 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0
L:1118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:1137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
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L:1175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
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L:1556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
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L:1613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:0
L:1656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
L:1680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
L:1704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
L:1728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
L:1752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0

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L:1776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0

L:1795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0